We claim:

1. A method for gene expression analysis comprising:

subjecting a gene to be analyzed to nucleic acid amplification in a single thermal cycle using a primer comprising a base sequence specifically hybridizing to a target gene, a primer comprising a base sequence identical to a second base sequence, a probe comprising a base sequence identical or complementary to a first base sequence, and labeled at one end with a fluorophore and at another end with a quencher, and thermostable DNA polymerase having 5'→3' exonuclease activity,

digesting the probe hybridized to the first base sequence by the thermostable DNA polymerase at the time of the nucleic acid amplification, and

detecting a fluorescence emitted by the released fluorophore, thereby assaying the amount of the product of the nucleic acid amplification,

wherein the gene to be analyzed is prepared by introducing the first base sequence and the second base sequence, which are nonspecific to the base sequence of the target gene, into the target gene so that the second base sequence is bound to a position closer to the 5' end than the first base sequence.

2. The method for gene expression analysis according to claim 1, wherein the gene to be analyzed is synthesized by introducing the first base sequence and the second base sequence into the target gene using a primer for introduction, which comprises the first base sequence, which is closer to the 5' end than the third base sequence comprising a sequence that specifically hybridizes to the target gene, and the second base sequence, which is closer to the 5' end than the first base sequence.

3. The method for gene expression analysis according to claim 1, wherein the gene to be analyzed is cDNA comprising the first base sequence and the second base sequence introduced therein by subjecting mRNA of the target gene to reverse transcription using a primer for introduction which comprises the first base sequence, which is closer to the 5' end than the third base sequence comprising a sequence that

specifically hybridizes to the target gene and the second base sequence, which is closer to the 5' end than the first base sequence.

4. The method for gene expression analysis according to claim 1, wherein samples derived from several specimens are simultaneously analyzed using two or more types of probes using one vessel for one target gene.

5. The method for gene expression analysis according to claim 4, wherein the Tm values of the two or more types of probes are substantially the same.

6. A kit for gene expression analysis comprising:

a probe comprising a sequence identical or complementary to a first base sequence, and labeled at one end with a fluorophore and at another end with a quencher, and

a primer comprising a sequence identical to a second base sequence and bound to a position closer to the 5' end than the first base sequence,

wherein the first base sequence and the second base sequence are nonspecific to a base sequence of a target gene and are introduced into the target gene.

7. The kit according to claim 6, wherein each of the two or more types of probes comprises several module sequences of 3 or 4 bases, the both terminal bases of each module sequence are identical to each other, and each probe is constituted by rearranging the order of module sequences having the identical terminal bases.